

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wiley, Steven R.
Goodwin, Raymond G.
- (ii) TITLE OF INVENTION: Cytokine that Induces Apoptosis
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
 - (B) STREET: 51 University Street
 - (C) CITY: Seattle
 - (D) STATE: WA
 - (E) COUNTRY: USA
 - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Apple 7.1
 - (D) SOFTWARE: Microsoft Word, Version 5.1a
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US --to be assigned--
 - (B) FILING DATE: 01-NOV-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/496,632
 - (B) FILING DATE: 29-JUN-1995
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Anderson, Kathryn A.
 - (B) REGISTRATION NUMBER: 32,172
 - (C) REFERENCE/DOCKET NUMBER: 2835-A
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (206) 587-0430
 - (B) TELEFAX: (206) 233-0644
 - (C) TELEX: 756822

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: huAIC

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 88..933

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTCACTGAC TATAAAAGAA TAGAGAAGGA AGGGCTTCAG TGACCGGCTG CCTGGCTGAC	60
TTACAGCAGT CAGACTCTGA CAGGATC ATG GCT ATG ATG GAG GTC CAG GGG	111
Met Ala Met Met Glu Val Gln Gly	
1 5	
GGA CCC AGC CTG GGA CAG ACC TGC GTG CTG ATC GTG ATC TTC ACA GTG	159
Gly Pro Ser Leu Gly Gln Thr Cys Val Leu Ile Val Ile Phe Thr Val	
10 15 20	
CTC CTG CAG TCT CTC TGT GTG GCT GTA ACT TAC GTG TAC TTT ACC AAC	207
Leu Leu Gln Ser Leu Cys Val Ala Val Thr Tyr Val Tyr Phe Thr Asn	
25 30 35 40	
GAG CTG AAG CAG ATG CAG GAC AAG TAC TCC AAA AGT GGC ATT GCT TGT	255
Glu Leu Lys Gln Met Gln Asp Lys Tyr Ser Lys Ser Gly Ile Ala Cys	
45 50 55	
TTC TTA AAA GAA GAT GAC AGT TAT TGG GAC CCC AAT GAC GAA GAG AGT	303
Phe Leu Lys Glu Asp Asp Ser Tyr Trp Asp Pro Asn Asp Glu Glu Ser	
60 65 70	
ATG AAC AGC CCC TGC TGG CAA GTC AAG TGG CAA CTC CGT CAG CTC GTT	351
Met Asn Ser Pro Cys Trp Gln Val Lys Trp Gln Leu Arg Gln Leu Val	
75 80 85	
AGA AAG ATG ATT TTG AGA ACC TCT GAG GAA ACC ATT TCT ACA GTT CAA	399
Arg Lys Met Ile Leu Arg Thr Ser Glu Glu Thr Ile Ser Thr Val Gln	
90 95 100	
GAA AAG CAA CAA AAT ATT TCT CCC CTA GTG AGA GAA AGA GGT CCT CAG	447
Glu Lys Gln Gln Asn Ile Ser Pro Leu Val Arg Glu Arg Gly Pro Gln	
105 110 115 120	
AGA GTA GCA GCT CAC ATA ACT GGG ACC AGA GGA AGA AGC AAC ACA TTG	495
Arg Val Ala Ala His Ile Thr Gly Thr Arg Gly Arg Ser Asn Thr Leu	
125 130 135	
TCT TCT CCA AAC TCC AAG AAT GAA AAG GCT CTG GGC CGC AAA ATA AAC	543
Ser Ser Pro Asn Ser Lys Asn Glu Lys Ala Leu Gly Arg Lys Ile Asn	
140 145 150	
TCC TGG GAA TCA TCA AGG AGT GGG CAT TCA TTC CTG AGC AAC TTG CAC	591
Ser Trp Glu Ser Ser Arg Ser Gly His Ser Phe Leu Ser Asn Leu His	
155 160 165	

TTG AGG AAT GGT GAA CTG GTC ATC CAT GAA AAA GGG TTT TAC TAC ATC	639
Leu Arg Asn Gly Glu Leu Val Ile His Glu Lys Gly Phe Tyr Tyr Ile	
170 175 180	
TAT TCC CAA ACA TAC TTT CGA TTT CAG GAG GAA ATA AAA GAA AAC ACA	687
Tyr Ser Gln Thr Tyr Phe Arg Phe Gln Glu Glu Ile Lys Glu Asn Thr	
185 190 195 200	
AAG AAC GAC AAA CAA ATG GTC CAA TAT ATT TAC AAA TAC ACA AGT TAT	735
Lys Asn Asp Lys Gln Met Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr	
205 210 215	
CCT GAC CCT ATA TTG TTG ATG AAA AGT GCT AGA AAT AGT TGT TGG TCT	783
Pro Asp Pro Ile Leu Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser	
220 225 230	
AAA GAT GCA GAA TAT GGA CTC TAT TCC ATC TAT CAA GGG GGA ATA TTT	831
Lys Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Ile Phe	
235 240 245	
GAG CTT AAG GAA AAT GAC AGA ATT TTT GTT TCT GTA ACA AAT GAG CAC	879
Glu Leu Lys Glu Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His	
250 255 260	
TTG ATA GAC ATG GAC CAT GAA GCC AGT TTT TTC GGG GCC TTT TTA GTT	927
Leu Ile Asp Met Asp His Glu Ala Ser Phe Phe Gly Ala Phe Leu Val	
265 270 275 280	
GGC TAA CTGACCTGGA AAGAAAAAGC AATAACCTCA AAGTGACTAT TCAGTTTTCA	983
Gly *	
GGATGATACA CTATGAAGAT GTTTCAAAAA ATCTGACCAA AACAAACAAA CAGAAAACAG	1043
AAAACAAAAA AACCTCTATG CAATCTGAGT AGAGCAGCCA CAACCAAAAA ATTCTACAAC	1103
ACACACTGTT CTGAAAGTGA CTCACCTATC CCAAGAAAAT GAAATTGCTG AAAGATCTTT	1163
CAGGACTCTA CCTCATATCA GTTTGCTAGC AGAAATCTAG AAGACTGTCA GCTTCCAAAC	1223
ATTAATGCAA TGGTTAACAT CTTCTGTCTT TATAATCTAC TCCTTGTAAG GACTGTAGAA	1283
GAAAGCGCAA CAATCCATCT CTCAAGTAGT GTATCACAGT AGTAGCCTCC AGGTTTCCTT	1343
AAGGGACAAC ATCCTTAAGT CAAAAGAGAG AAGAGGCACC ACTAAAAGAT CGCAGTTTGC	1403
CTGGTGCAGT GGCTCACACC TGTAATCCCA ACATTTTGGG AACCCAAGGT GGGTAGATCA	1463
CGAGATCAAG AGATCAAGAC CATAGTGACC AACATAGTGA AACCCCATCT CTAAGTAAAG	1523
TGCAAAAATT AGCTGGGTGT GTTGGCACAT GCCTGTAGTC CCAGCTACTT GAGAGGCTGA	1583
GGCAGGAGAA TCGTTTGAAC CCGGGAGGCA GAGGTTGCAG TGTGGTGAGA TCATGCCACT	1643
ACACTCCAGC CTGGCGACAG AGCGAGACTT GGTTTCAAAA AAAAAAAAAA AAAAAAACTT	1703
CAGTAAGTAC GTGTTATTTT TTTCAATAAA ATTCTATTAC AGTATGTC	1751

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Met	Met	Glu	Val	Gln	Gly	Gly	Pro	Ser	Leu	Gly	Gln	Thr	Cys	
1				5					10					15		
Val	Leu	Ile	Val	Ile	Phe	Thr	Val	Leu	Leu	Gln	Ser	Leu	Cys	Val	Ala	
			20					25					30			
Val	Thr	Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	Gln	Met	Gln	Asp	Lys	
		35					40					45				
Tyr	Ser	Lys	Ser	Gly	Ile	Ala	Cys	Phe	Leu	Lys	Glu	Asp	Asp	Ser	Tyr	
	50					55					60					
Trp	Asp	Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	Pro	Cys	Trp	Gln	Val	
65					70				75						80	
Lys	Trp	Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Met	Ile	Leu	Arg	Thr	Ser	
				85					90					95		
Glu	Glu	Thr	Ile	Ser	Thr	Val	Gln	Glu	Lys	Gln	Gln	Asn	Ile	Ser	Pro	
			100					105					110			
Leu	Val	Arg	Glu	Arg	Gly	Pro	Gln	Arg	Val	Ala	Ala	His	Ile	Thr	Gly	
		115				120						125				
Thr	Arg	Gly	Arg	Ser	Asn	Thr	Leu	Ser	Ser	Pro	Asn	Ser	Lys	Asn	Glu	
	130					135					140					
Lys	Ala	Leu	Gly	Arg	Lys	Ile	Asn	Ser	Trp	Glu	Ser	Ser	Arg	Ser	Gly	
145					150					155					160	
His	Ser	Phe	Leu	Ser	Asn	Leu	His	Leu	Arg	Asn	Gly	Glu	Leu	Val	Ile	
				165					170					175		
His	Glu	Lys	Gly	Phe	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	Tyr	Phe	Arg	Phe	
			180					185					190			
Gln	Glu	Glu	Ile	Lys	Glu	Asn	Thr	Lys	Asn	Asp	Lys	Gln	Met	Val	Gln	
		195					200					205				
Tyr	Ile	Tyr	Lys	Tyr	Thr	Ser	Tyr	Pro	Asp	Pro	Ile	Leu	Leu	Met	Lys	
	210					215					220					
Ser	Ala	Arg	Asn	Ser	Cys	Trp	Ser	Lys	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	
225					230					235					240	
Ser	Ile	Tyr	Gln	Gly	Gly	Ile	Phe	Glu	Leu	Lys	Glu	Asn	Asp	Arg	Ile	
				245					250					255		

Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu Ala
 260 265 270

Ser Phe Phe Gly Ala Phe Leu Val Gly *
 275 280

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1521 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HuAIC-dv

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 78..383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AATTC	CGGAA	TAGAGA	AAGGA	AGGGCT	TCAG	TGACCG	GCTG	CCTGG	CTGAC	TTACAG	CAGT	60				
CAGACT	CTGA	CAGGAT	C	ATG	GCT	ATG	ATG	GAG	GTC	CAG	GGG	GGA	CCC	AGC	110	
				Met	Ala	Met	Met	Glu	Val	Gln	Gly	Gly	Pro	Ser		
				1				5					10			
CTG	GGA	CAG	ACC	TGC	GTG	CTG	ATC	GTG	ATC	TTC	ACA	GTG	CTC	CTG	CAG	158
Leu	Gly	Gln	Thr	Cys	Val	Leu	Ile	Val	Ile	Phe	Thr	Val	Leu	Leu	Gln	
				15				20					25			
TCT	CTC	TGT	GTG	GCT	GTA	ACT	TAC	GTG	TAC	TTT	ACC	AAC	GAG	CTG	AAG	206
Ser	Leu	Cys	Val	Ala	Val	Thr	Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	
				30				35					40			
CAG	ATG	CAG	GAC	AAG	TAC	TCC	AAA	AGT	GGC	ATT	GCT	TGT	TTC	TTA	AAA	254
Gln	Met	Gln	Asp	Lys	Tyr	Ser	Lys	Ser	Gly	Ile	Ala	Cys	Phe	Leu	Lys	
				45				50					55			
GAA	GAT	GAC	AGT	TAT	TGG	GAC	CCC	AAT	GAC	GAA	GAG	AGT	ATG	AAC	AGC	302
Glu	Asp	Asp	Ser	Tyr	Trp	Asp	Pro	Asn	Asp	Glu	Glu	Ser	Met	Asn	Ser	
				60				65					70			
CCC	TGC	TGG	CAA	GTC	AAG	TGG	CAA	CTC	CGT	CAG	CTC	GTT	AGA	AAG	ACT	350
Pro	Cys	Trp	Gln	Val	Lys	Trp	Gln	Leu	Arg	Gln	Leu	Val	Arg	Lys	Thr	
				80				85					90			
CCA	AGA	ATG	AAA	AGG	CTC	TGG	GCC	GCA	AAA	TAA	ACTCCT	GCGGA	ATCAT	CAAGG	403	
Pro	Arg	Met	Lys	Arg	Leu	Trp	Ala	Ala	Lys	*						
				95				100								

AGTGGGCATT CATTCCTGAG CAACTTGCAC TTGAGGAATG GTGAACTGGT CATCCATGAA 463
 AAAGGGTTTT ACTACATCTA TTCCCAAACA TACTTTTCGAT TTCAGGAGGA AATAAAAGAA 523
 AACACAAAGA ACGACAAACA AATGGTCCAA TATATTTACA AATACACAAG TTATCCTGAC 583
 CCTATATTGT TGATGAAAAG TGCTAGAAAT AGTTGTTGGT CTAAAGATGC AGAATATGGA 643
 CTCTATTCCA TCTATCAAGG GGGAATATTT GAGCTTAAGG AAAATGACAG AATTTTTGTT 703
 TCTGTAACAA ATGAGCACTT GATAGACATG GACCATGAAG CCAGTTTTTT CGGGGCCTTT 763
 TTAGTTGGCT AACTGACCTG GAAAGAAAAA GCAATAACCT CAAAGTGACT ATTCAGTTTT 823
 CAGGATGATA CACTATGAAG ATGTTTCAAA AAATCTGACC AAAACAAACA AACAGAAAAC 883
 AGAAAACAAA AAAACCTCTA TGCAATCTGA GTAGAGCAGC CACAACCAAA AAATTCTACA 943
 ACACACACTG TTCTGAAAGT GACTCACTTA TCCCAAGAGA ATGAAATTGC TGAAAGATCT 1003
 TTCAGGACTC TACCTCATAT CAGTTTGCTA GCAGAAATCT AGAAGACTGT CAGCTTCCAA 1063
 ACATTAATGC AGTGGTTAAC ATCTTCTGTC TTTATAATCT ACTCCTTGTA AAGACTGTAG 1123
 AAGAAAGCGC AACAATCCAT CTCTCAAGTA GTGTATCACA GTAGTAGCCT CCAGGTTTCC 1183
 TTAAGGGACA ACATCCTTAA GTCAAAAGAG AGAAGAGGCA CCACTAAAAG ATCGCAGTTT 1243
 GCCTGGTGCA GTGGCTCACA CCTGTAATCC CAACATTTTG GGAACCCAAG GTGGGTAGAT 1303
 CACGAGATCA AGAGATCAAG ACCATAGTGA CCAACATAGT GAAACCCCAT CTCTACTGAA 1363
 AGTGCAAAAA TTAGCTGGGT GTGTTGGCAG ATGCCTGTAG TCCCAGCTAC TTGAGAGGCT 1423
 GAGGCAGGAG AATCGTTTGA ACCCGGGAGG CAGAGGTTGC AGTGTGGTGA GATCATGCCA 1483
 CTACACTCCA GCCTGGCGAC AGAGCGAGAC TTGGTTTC 1521

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Met	Met	Glu	Val	Gln	Gly	Gly	Pro	Ser	Leu	Gly	Gln	Thr	Cys
1				5					10					15	
Val	Leu	Ile	Val	Ile	Phe	Thr	Val	Leu	Leu	Gln	Ser	Leu	Cys	Val	Ala
			20					25					30		
Val	Thr	Tyr	Val	Tyr	Phe	Thr	Asn	Glu	Leu	Lys	Gln	Met	Gln	Asp	Lys
		35					40					45			

GTT AAG AGG CAA CTG TAT CAG CTC ATT GAA GAG GTG ACT TTG AGA ACC	343
Val Lys Arg Gln Leu Tyr Gln Leu Ile Glu Glu Val Thr Leu Arg Thr	
85 90 95	
TTT CAG GAC ACC ATT TCT ACA GTT CCA GAA AAG CAG CTA AGT ACT CCT	391
Phe Gln Asp Thr Ile Ser Thr Val Pro Glu Lys Gln Leu Ser Thr Pro	
100 105 110 115	
CCC TTG CCC AGA GGT GGA AGA CCT CAG AAA GTG GCA GCT CAC ATT ACT	439
Pro Leu Pro Arg Gly Gly Arg Pro Gln Lys Val Ala Ala His Ile Thr	
120 125 130	
GGG ATC ACT CGG AGA AGC AAC TCA GCT TTA ATT CCA ATC TCC AAG GAT	487
Gly Ile Thr Arg Arg Ser Asn Ser Ala Leu Ile Pro Ile Ser Lys Asp	
135 140 145	
GGA AAG ACC TTA GGC CAG AAG ATT GAA TCC TGG GAG TCC TCT CGG AAA	535
Gly Lys Thr Leu Gly Gln Lys Ile Glu Ser Trp Glu Ser Ser Arg Lys	
150 155 160 265	
GGG CAT TCA TTT CTC AAC CAC GTG CTC TTT AGG AAT GGA GAG CTG GTC	583
Gly His Ser Phe Leu Asn His Val Leu Phe Arg Asn Gly Glu Leu Val	
165 170 175	
ATC GAG CAG GAG GGC CTG TAT TAC ATC TAT TCC CAA ACA TAC TTC CGA	631
Ile Glu Gln Glu Gly Leu Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg	
180 185 190 195	
TTT CAG GAA GCT GAA GAC GCT TCC AAG ATG GTC TCA AAG GAC AAG GTG	679
Phe Gln Glu Ala Glu Asp Ala Ser Lys Met Val Ser Lys Asp Lys Val	
200 205 210	
AGA ACC AAA CAG CTG GTG CAG TAC ATC TAC AAG TAC ACC AGC TAT CCG	727
Arg Thr Lys Gln Leu Val Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro	
215 220 225	
GAT CCC ATA GTG CTC ATG AAG AGC GCC AGA AAC AGC TGT TGG TCC AGA	775
Asp Pro Ile Val Leu Met Lys Ser Ala Arg Asn Ser Cys Trp Ser Arg	
230 235 240	
GAT GCC GAG TAC GGA CTG TAC TCC ATC TAT CAG GGA GGA TTG TTC GAG	823
Asp Ala Glu Tyr Gly Leu Tyr Ser Ile Tyr Gln Gly Gly Leu Phe Glu	
245 250 255	
CTA AAA AAA AAT GAC AGG ATT TTT GTT TCT GTG ACA AAT GAA CAT TTG	871
Leu Lys Lys Asn Asp Arg Ile Phe Val Ser Val Thr Asn Glu His Leu	
260 265 270 275	
ATG GAC CTG GAT CAA GAA GCC AGC TTC TTT GGA GCC TTT TTA ATT AAC	919
Met Asp Leu Asp Gln Glu Ala Ser Phe Phe Gly Ala Phe Leu Ile Asn	
280 285 290	
TAAATGACCA GTAAAGATCA AACACAGCCC TAAAGTACCC AGTAATCTTC TAGGTTGAAG	979
GCATGCCTGG AAAGCGACTG AACTGGTTAG GATATGGCCT GGCTGTAGAA ACCTCAGGAC	1039
AGATGTGACA GAAAGGCAGC TGGAAGTCAG CAGCGACAGG CCAACAGTCC AGCCACAGAC	1099
ACTTTCGGTG TTTCATCGAG AGACTTGCTT TCTTTCCGCA AAATGAGATC ACTGTAGCCT	1159

TTCAATGATC TACCTGGTAT CAGTTTGCAG AGATCTAGAA GACGTCCAGT TTCTAAATAT 1219
 TTATGCAACA ATTGACAATT TTCACCTTTG TTATCTGGTC CAGGGGTGTA AAGCCAAGTG 1279
 CTCACAAGCT GTGTGCAGAC CAGGATAGCT ATGAATGCAG GTCAGCATAA AAATCACAGA 1339
 ATATCTCACC TACTAAAAAA AAAAAAA 1366

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Pro	Ser	Ser	Gly	Ala	Leu	Lys	Asp	Leu	Ser	Phe	Ser	Gln	His	Phe	1	5	10	15
Arg	Met	Met	Val	Ile	Cys	Ile	Val	Leu	Leu	Gln	Val	Leu	Leu	Gln	Ala	20	25	30	
Val	Ser	Val	Ala	Val	Thr	Tyr	Met	Tyr	Phe	Thr	Asn	Glu	Met	Lys	Gln	35	40	45	
Leu	Gln	Asp	Asn	Tyr	Ser	Lys	Ile	Gly	Leu	Ala	Cys	Phe	Ser	Lys	Thr	50	55	60	
Asp	Glu	Asp	Phe	Trp	Asp	Ser	Thr	Asp	Gly	Glu	Ile	Leu	Asn	Arg	Pro	65	70	75	80
Cys	Leu	Gln	Val	Lys	Arg	Gln	Leu	Tyr	Gln	Leu	Ile	Glu	Glu	Val	Thr	85	90	95	
Leu	Arg	Thr	Phe	Gln	Asp	Thr	Ile	Ser	Thr	Val	Pro	Glu	Lys	Gln	Leu	100	105	110	
Ser	Thr	Pro	Pro	Leu	Pro	Arg	Gly	Gly	Arg	Pro	Gln	Lys	Val	Ala	Ala	115	120	125	
His	Ile	Thr	Gly	Ile	Thr	Arg	Arg	Ser	Asn	Ser	Ala	Leu	Ile	Pro	Ile	130	135	140	
Ser	Lys	Asp	Gly	Lys	Thr	Leu	Gly	Gln	Lys	Ile	Glu	Ser	Trp	Glu	Ser	145	150	155	160
Ser	Arg	Lys	Gly	His	Ser	Phe	Leu	Asn	His	Val	Leu	Phe	Arg	Asn	Gly	165	170	175	
Glu	Leu	Val	Ile	Glu	Gln	Glu	Gly	Leu	Tyr	Tyr	Ile	Tyr	Ser	Gln	Thr	180	185	190	
Tyr	Phe	Arg	Phe	Gln	Glu	Ala	Glu	Asp	Ala	Ser	Lys	Met	Val	Ser	Lys	195	200	205	

Asp	Lys	Val	Arg	Thr	Lys	Gln	Leu	Val	Gln	Tyr	Ile	Tyr	Lys	Tyr	Thr
210						215					220				
Ser	Tyr	Pro	Asp	Pro	Ile	Val	Leu	Met	Lys	Ser	Ala	Arg	Asn	Ser	Cys
225					230					235					240
Trp	Ser	Arg	Asp	Ala	Glu	Tyr	Gly	Leu	Tyr	Ser	Ile	Tyr	Gln	Gly	Gly
				245					250					255	
Leu	Phe	Glu	Leu	Lys	Lys	Asn	Asp	Arg	Ile	Phe	Val	Ser	Val	Thr	Asn
			260					265					270		
Glu	His	Leu	Met	Asp	Leu	Asp	Gln	Glu	Ala	Ser	Phe	Phe	Gly	Ala	Phe
		275					280						285		
Leu	Ile	Asn													
		290													

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: FLAG peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys
1							5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: not relevant
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: conserved peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Val Val Xaa Xaa Xaa Gly Leu Tyr Tyr Val Tyr Xaa Gln Val Xaa
1 5 10 15
Phe

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: CMV leader

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Arg Arg Leu Trp Ile Leu Ser Leu Leu Ala Val Thr Leu Thr
1 5 10 15
Val Ala Leu Ala Ala Pro Ser Gln Lys Ser Lys Arg Arg Thr Ser Ser
20 25 30